



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]

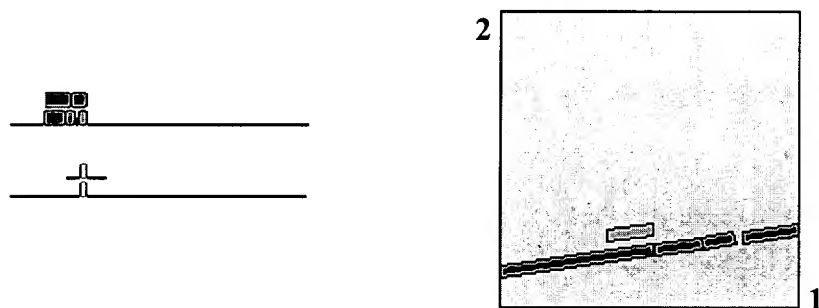
Matrix **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☒ View option **Standard**
 Masking character option **X for protein, n for nucleotide** Masking color option **Black**
☐ Show CDS translation **Align**

Sequence 1: gi|47117817|sp|O75376|NCOR1_HUMAN Nuclear receptor corepressor 1 (N-CoR1) (N-CoR).

Length = 357 (312 .. 668) **SEQ ID NO: 1**

Sequence 2: gi|4559298|gb|AAD22973.1|AF125672.1 silencing mediator of retinoic acid and thyroid hormone receptor extended isoform [Homo sapiens]

Length = 2507 (1 .. 2507)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 363 bits (933), Expect = 7e-99

Identities = 229/363 (63%), Positives = 290/363 (79%), Gaps = 17/363 (4%)

Query	312	DQLMEAWKVKVDRIENNPRRKAKESKTREYYEKQFPXXXXXXXXXXXXXXXXXXXXGAGLSA	371
		DQLMEAWKVKV+RIENNPRR+AKESK REYYEKQFPEIRKQRE QER QRVGQRG+GLS	
Sbjct	303	DQLMEAWKVKVERIENNPRRRAKESKREYYEKQFPEIRKQRELQERMQRVGQRGSGLSM	362
Query	372	TIARSEHEISEIIDGLSEQENNEKQMRQLSVIPPMFDAEQRRVKFINMNGLMEDPMKVY	431
		+ ARSEHE+SEIIDGLSEQEN EKQMRQL+VIPPM++DA+Q+R+KFINMNGLM DPMKVY	
Sbjct	363	SPARSEHEVSEIIDGLSEQENLEKQMRQLAVIPPMPLYDADQRIKFINMNGLMADPMKVY	422
Query	432	KDRQFMNVWTDHEKEIFKDKFIQHPKNFGLIASYLERKSVPCVLYYYLTCKKNENYKALV	491
		KDRQ MN+W++ EKE F++KF+QHPKNFGLIAS+LERK+V +CVLYYYLTCKKNENYK+LV	
Sbjct	423	KDRQVMNMWSEQEKETFREKFMQHPKNFGLIASFLERKTVACVLYYYLTCKKNENYKSLV	482
Query	492	RRNYGKRRGRNQIARPSQXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	551

```

Sbjct  483  RR+Y +RRG++QQ  +  Q+++ ++++++  ++++++EK+ E+E +++E+  E  +K
RRSY-RRRGKSQQQQQQQQQQQQQQQQQQQPMRSSHQEEKDEKEKEKEAEKEEEKPEVENDK  541

Query  552  XXI-----DGXXXXXXXXXXXXPRGRKTANSQGRRKGRITRSMNXXXXXXXXXXXXXXXXX  605
+ +      D + E+ +E+E  +GRKTANSQGRRKGRITRSM N      A
Sbjct  542  EDLLKEKTDDTSGEDNDEKEAVASKGRKTANSQGRRKGRITRSMAN-----EANS  591

Query  606  XXXXXXXXXXXXXXXXXXXXXXXRWTEEMEVAKKGLVEHGRNWAAIAKMVGTKSEAQCCKNF  665
E      E S E  E+SRWTEEME AKKGL+EHGRNW+AIA+MVG+K+ +QCCKNF
Sbjct  592  EEAITPQQAELASMELNESSRWTEEMEETAKKGLLEHGRNWSAIARMVGSKTVSQCKNF  651

Query  666  YFN  668
YFN
Sbjct  652  YFN  654

```



Score = 39.3 bits (90), Expect = 0.40
 Identities = 16/55 (29%), Positives = 31/55 (56%), Gaps = 0/55 (0%)

```

Query  440  WTDHEKEIFKDKFIQHPKNFGLIASYLERKSVPCVLYYYLTKKKNENYKALVRRN  494
WT+ E E K  ++H +N+  IA  +  K+V  C  +Y+  KK +N  +++++
Sbjct  614  WTEEMEETAKKGLLEHGRNWSAIARMVGSKTVSQCKNFYFNYKKRQNLDEILQQH  668

```

CPU time: 0.06 user secs. 0.01 sys. secs 0.07 total secs.

Lambda K H
 0.316 0.131 0.384

Gapped
 Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Sequences: 1
 Number of Hits to DB: 4056
 Number of extensions: 2656
 Number of successful extensions: 6
 Number of sequences better than 10.0: 1
 Number of HSP's gapped: 2
 Number of HSP's successfully gapped: 2
 Length of query: 357
 Length of database: 1,199,905,207
 Length adjustment: 134
 Effective length of query: 223
 Effective length of database: 1,199,905,073
 Effective search space: 267578831279
 Effective search space used: 267578831279
 Neighboring words threshold: 9
 X1: 16 (7.3 bits)
 X2: 129 (49.7 bits)
 X3: 129 (49.7 bits)

S1: 41 (21.6 bits)
S2: 78 (34.7 bits)